

*Exhibit A***Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]**

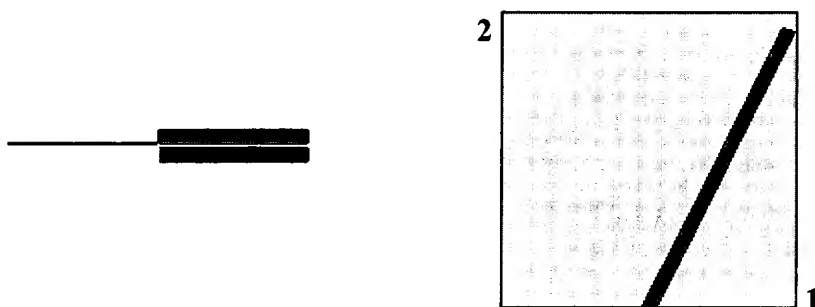
Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ View option **Standard**  
Masking character option **X for protein, n for nucleotide** Masking color option **Black**  
☐ Show CDS translation **Align**

**Sequence 1:** lcl|seq\_1

Length = 28 (1 .. 28)

**Sequence 2:** lcl|seq\_2

Length = 14 (1 .. 14)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 38.1 bits (87), Expect = 0.094

Identities = 14/14 (100%), Positives = 14/14 (100%), Gaps = 0/14 (0%)

```
Query 15 AGCKNFFWKTFTSC 28
          AGCKNFFWKTFTSC
Sbjct 1  AGCKNFFWKTFTSC 14
```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda	K	H
0.320	0.125	0.434

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Sequences: 1  
Number of Hits to DB: 16  
Number of extensions: 5  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Length of query: 28  
Length of database: 1,129,354,045  
Length adjustment: 3  
Effective length of query: 25  
Effective length of database: 1,129,354,042  
Effective search space: 28233851050  
Effective search space used: 28233851050  
Neighboring words threshold: 9  
X1: 16 ( 7.4 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 41 (21.9 bits)  
S2: 70 (31.6 bits)